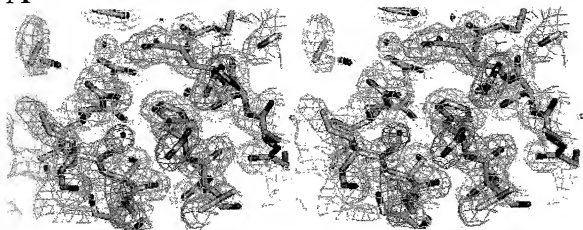


A



B

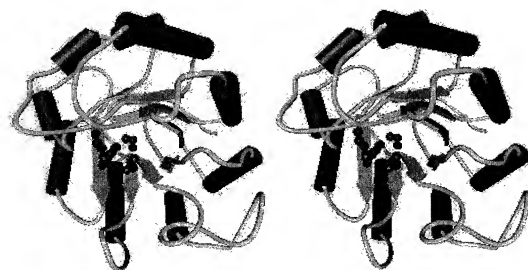


FIGURE 1A&B

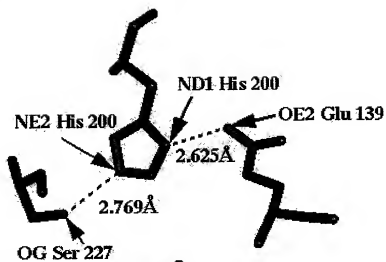
C



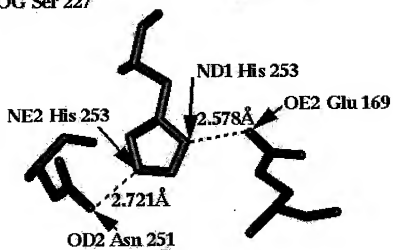
FIGURE 1 c

10066374-000000

A



B



C

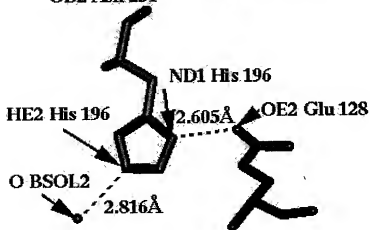


FIGURE 2 A, B
& C

FIGURE 3A

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bacillus sp.
 - (C) INDIVIDUAL ISOLATE: CBS 670.93
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1..78
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 79..1404
 - (D) OTHER INFORMATION: /function= "endoglucanase"
/EC_number= 3.2.1.4
/product= "BCE103 cellulase"
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AAA AAG ATA ACT ACT ATT TTT GCC GTA TTG CTC ATG ACA TTG GCG
 Met Lys Lys Ile Thr Thr Ile Phe Ala Val Leu Leu Met Thr Leu Ala
 -26 -25 -20 -15

FIGURE 3B

TTG TTC AGT ATA GGA AAC ACG ACA GCG GCT GAT GAT TAT TCA GTT GTA Leu Phe Ser Ile Gly Asn Thr Thr Ala Ala Asp Tyr Ser Val Val -10 -5 1 5	96
GAG GAA CAT GGG CAA CTA AGT ATT AGT AAC GGT GAA TTA GTC AAT GAA Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu Val Asn Glu 10 15 20	144
CGA GGC GAA CAA GTT CAG TTA AAA GGG ATG AGT TCC CAT GGT TTG CAA Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His Gly Leu Gln 25 30 35	192
TGG TAC GGT CAA TTT GTA AAC TAT GAA AGC ATG AAA TGG CTA AGA GAT Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp Leu Arg Asp 40 45 50	240
GAT TGG GGA ATA ACT GTA TTC CGA GCA GCA ATG TAT ACC TCT TCA GGA Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr Ser Ser Gly 55 60 65 70	288
GGA TAT ATT GAC GAT CCA TCA GTA AAG GAA AAA GTA AAA GAG ACT GTT Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys Glu Thr Val 75 80 85	336
GAG GCT GCG ATA GAC CTT GGC ATA TAT GTG ATC ATT GAT TGG CAT ATC Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp Trp His Ile 90 95 100	384
CTT TCA GAC AAT GAC CCG AAT ATA TAT AAA GAA GAA GCG AAG GAT TTC Leu Ser Asp Asn Asp Pro Asp Ile Tyr Lys Glu Glu Ala Lys Asp Phe 105 110 115	432
TTT GAT GAA ATG TCA GAG TTG TAT GGA GAC TAT CCG AAT GTG ATA TAC Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn Val Ile Tyr 120 125 130	480
GAA ATT GCA AAT GAA CCG AAT GGT AGT GAT GTT ACG TGG GAC AAT CAA Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp Asp Asn Gln 135 140 145 150	528
ATA AAA CCG TAT GCA GAA GAA GTG ATT CCG GTT ATT CGT GAC AAT GAC Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg Asp Asn Asp 155 160 165	576
CCT AAT AAC ATT GTT ATT GTA GGT ACA GGT ACA TGG AGT CAG GAT GTC Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser Gln Asp Val 170 175 180	624
CAT CAT GCA GCC GAT AAT CAG CTT GCA GAT CCT AAC GTC ATG TAT GCA His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val Met Tyr Ala 185 190 195	672
TTT CAT TTT TAT GCA GGA ACA CAT GGA CAA AAT TTA CGA GAC CAA GTA Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg Asp Gln Val 200 205 210	720
GAT TAT GCA TTA GAT CAA GGA GCA GCG ATA TTT GTT AGT GAA TGG GGG Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser Glu Trp Gly 215 220 225 230	768
ACA AGT GCA GCT ACA GGT GAT GGT GGT GTG TTT TTA GAT GAA GCA CAA Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp Glu Ala Gln 235 240 245	816

FIGURE 3C

GTG TGG ATT GAC TTT ATG GAT GAA AGA AAT TTA AGC TGG GCC AAC TGG Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp Ala Asn Trp 250 255 260	864
TCT CTA ACG CAT AAG GAT GAG TCA TCT GCA GCG TTA ATG CCA GGT GCA Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met Pro Gly Ala 265 270 275	912
AAT CCA ACT GGT GGT TGG ACA GAG GCT GAA CTA TCT CCA TCT GGT ACA Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro Ser Gly Thr 280 285 290	960
TTT GTG AGG GAA AAA ATA AGA GAA TCA GCA TCT ATT CCG CCA AGC GAT Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Ile Pro Pro Ser Asp 295 300 305 310	1008
CCA ACA CCG CCA TCT GAT CCA GGA GAA CCG GAT CCA GGA GAA CCG GAT Pro Thr Pro Pro Ser Asp Pro Gly Glu Pro Asp Pro Gly Glu Pro Asp 315 320 325	1056
CCA ACG CCC CCA AGT GAT CCA GGA GAG TAT CCA GCA TGG GAT TCA AAT Pro Thr Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn 330 335 340	1104
CAA ATT TAC ACA AAT GAA ATT GTG TAT CAT AAC GGT CAG TTA TGG CAA Gln Ile Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln 345 350 355	1152
GCG AAA TGG TGG ACA CAA AAT CAA GAG CCA GGT GAC CCA TAC GGT CCG Ala Lys Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro 360 365 370	1200
TGG GAA CCA CTC AAA TCT GAC CCA GAT TCA GGA GAA CCG GAT CCA ACG Trp Glu Pro Leu Lys Ser Asp Pro Asp Ser Gly Glu Pro Asp Pro Thr 375 380 385 390	1248
CCC CCA AGT GAT CCA GGA GAG TAT CCA GCA TGG GAT TCA AAT CAA ATT Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn Gln Ile 395 400 405	1296
TAC ACA AAT GAA ATT GTG TAC CAT AAC GGC CAG CTA TGG CAA GCA AAA Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln Ala Lys 410 415 420	1344
TGG TGG ACA CAA AAT CAA GAG CCA GGT GAC CCA TAT GGT CCG TGG GAA Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro Trp Glu 425 430 435	1392
CCA CTC AAT TAA Pro Leu Asn 440	1404

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Met	Lys	Lys	Ile	Thr	Thr	Ile	Phe	Ala	Val	Leu	Leu	Met	Thr	Leu	Ala
-26	-25					-20					-15				
Leu	Phe	Ser	Ile	Gly	Asn	Thr	Thr	Ala	Ala	Asp	Asp	Tyr	Ser	Val	Val
-10					-5					1				5	
Glu	Glu	His	Gly	Gln	Leu	Ser	Ile	Ser	Asn	Gly	Glu	Leu	Val	Asn	Glu
			10					15					20		
Arg	Gly	Glu	Gln	Val	Gln	Leu	Lys	Gly	Met	Ser	Ser	His	Gly	Leu	Gln
		25					30					35			
Trp	Tyr	Gly	Gln	Phe	Val	Asn	Tyr	Glu	Ser	Met	Lys	Trp	Leu	Arg	Asp
	40					45					50				
Asp	Trp	Gly	Ile	Thr	Val	Phe	Arg	Ala	Ala	Met	Tyr	Thr	Ser	Ser	Gly
55					60					65					70
Gly	Tyr	Ile	Asp	Asp	Pro	Ser	Val	Lys	Glu	Lys	Val	Lys	Glu	Thr	Val
			75						80					85	
Glu	Ala	Ala	Ile	Asp	Leu	Gly	Ile	Tyr	Val	Ile	Ile	Asp	Trp	His	Ile
			90					95					100		
Leu	Ser	Asp	Asn	Asp	Pro	Asn	Ile	Tyr	Lys	Glu	Glu	Ala	Lys	Asp	Phe
		105					110					115			
Phe	Asp	Glu	Met	Ser	Glu	Leu	Tyr	Gly	Asp	Tyr	Pro	Asn	Val	Ile	Tyr
	120					125					130				
Glu	Ile	Ala	Asn	Glu	Pro	Asn	Gly	Ser	Asp	Val	Thr	Trp	Asp	Asn	Gln
135					140					145					150
Ile	Lys	Pro	Tyr	Ala	Glu	Glu	Val	Ile	Pro	Val	Ile	Arg	Asp	Asn	Asp
				155					160					165	
Pro	Asn	Asn	Ile	Val	Ile	Val	Gly	Thr	Gly	Thr	Trp	Ser	Gln	Asp	Val
		170					175						180		
His	His	Ala	Ala	Asp	Asn	Gln	Leu	Ala	Asp	Pro	Asn	Val	Met	Tyr	Ala
		185					190					195			
Phe	His	Phe	Tyr	Ala	Gly	Thr	His	Gly	Gln	Asn	Leu	Arg	Asp	Gln	Val
	200					205					210				
Asp	Tyr	Ala	Leu	Asp	Gln	Gly	Ala	Ala	Ile	Phe	Val	Ser	Glu	Trp	Gly
215				220						225				230	
Thr	Ser	Ala	Ala	Thr	Gly	Asp	Gly	Gly	Val	Phe	Leu	Asp	Glu	Ala	Gln
			235					240					245		
Val	Trp	Ile	Asp	Phe	Met	Asp	Glu	Arg	Asn	Leu	Ser	Trp	Ala	Asn	Trp
		250						255					260		
Ser	Leu	Thr	His	Lys	Asp	Glu	Ser	Ser	Ala	Ala	Leu	Met	Pro	Gly	Ala
	265					270						275			
Asn	Pro	Thr	Gly	Gly	Trp	Thr	Glu	Ala	Glu	Leu	Ser	Pro	Ser	Gly	Thr
		280				285					290				
Phe	Val	Arg	Glu	Lys	Ile	Arg	Glu	Ser	Ala	Ser	Ile	Pro	Pro	Ser	Asp
295				300						305					310

FIGURE 3E

Pro Thr Pro Pro Ser Asp Pro Gly Glu Pro Asp Pro Gly Glu Pro Asp
 315 320 325

Pro Thr Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn
 330 335 340

Gln Ile Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln
 345 350 355

Ala Lys Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro
 360 365 370

Trp Glu Pro Leu Lys Ser Asp Pro Asp Ser Gly Glu Pro Asp Pro Thr
 375 380 385 390

Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn Gln Ile
 395 400 405

Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln Ala Lys
 410 415 420

Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro Trp Glu
 425 430 435

Pro Leu Asn
 440